CRF Errors Corrected by the STIC System Branch

Serial Number: 07/952,640A

CRF Processing Date: 7/29/93
Edited by: _____
Verified by: DS 7/30/93 (STIC staff)

#14

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Inserted a space between the last nucleic designator and the nucleic number for sequences:
_____

☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☑ Other: Deleted all hard page break codes
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

5/26/93

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/07/952,640A*

DATE: 07/29/93
TIME: 14:46:42

INPUT SET: S1104.raw

Au 1806

Hard page break codes throughout. Delete all (These don't convert into ASCII appropriately)

```
 1                              SEQUENCE LISTING
 2
 3      (1)     General Information:
 4
 5          (i) APPLICANT: CROWE, JAMES SCOTT
 6                         LEWIS, ALAN PETER
 7
 8         (ii) TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
 9
10        (iii) NUMBER OF SEQUENCES: 46
11
12         (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
14              (B) STREET: 555 THIRTEENTH ST. N.W.
15              (C) CITY: WASHINGTON
16              (D) STATE: D. C.
17              (E) COUNTRY: U.S.
18              (F) ZIP: 20004
19
20          (v) COMPUTER READABLE FORM:
21              (A) MEDIUM TYPE: Floppy disk
22              (B) COMPUTER: IBM PC compatible
23              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24              (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26         (vi) CURRENT APPLICATION DATA:
27              (A) APPLICATION NUMBER: US 07/952640
28              (B) FILING DATE: 01-DEC-1992
29              (C) CLASSIFICATION:
30
31       (viii) ATTORNEY/AGENT INFORMATION:
32              (A) NAME: ERNST, BARBARA G
33              (B) REGISTRATION NUMBER: 30,377
34              (C) REFERENCE/DOCKET NUMBER: 1808-118
35
36         (ix) TELECOMMUNICATION INFORMATION:
37              (A) TELEPHONE: (202) 783-6040
38              (B) TELEFAX: (202) 783-6031
39
40
41      (2) INFORMATION FOR SEQ ID NO:1:
42
43          (i) SEQUENCE CHARACTERISTICS:
44              (A) LENGTH: 24 base pairs
45              (B) TYPE: nucleic acid
46              (C) STRANDEDNESS: single
47              (D) TOPOLOGY: linear
48
49         (ii) MOLECULE TYPE: DNA (genomic)
50
51         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
```

```
52
53     GACATTCAGC TGACCCAGTC TCCA                                        24
54
55     (2) INFORMATION FOR SEQ ID NO:2:
56
57         (i) SEQUENCE CHARACTERISTICS:
58             (A) LENGTH: 24 base pairs
59             (B) TYPE: nucleic acid
60             (C) STRANDEDNESS: single
61             (D) TOPOLOGY: linear
62
63         (ii) MOLECULE TYPE: DNA (genomic)
64
65         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
66
67     GATCAAGCTT CTAACACTCT CCCC                                        24
68
69     (2) INFORMATION FOR SEQ ID NO:3:
70
71         (i) SEQUENCE CHARACTERISTICS:
72             (A) LENGTH: 34 base pairs
73             (B) TYPE: nucleic acid
74             (C) STRANDEDNESS: single
75             (D) TOPOLOGY: linear
76
77         (ii) MOLECULE TYPE: DNA (genomic)
78
79         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
80
81     GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA                             34
82
83     (2) INFORMATION FOR SEQ ID NO:4:
84
85         (i) SEQUENCE CHARACTERISTICS:
86             (A) LENGTH: 16 base pairs
87             (B) TYPE: nucleic acid
88             (C) STRANDEDNESS: single
89             (D) TOPOLOGY: linear
90
91         (ii) MOLECULE TYPE: DNA (genomic)
92
93         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
94
95     AACAGCTATG ACCATG                                                 16
96
97     (2) INFORMATION FOR SEQ ID NO:5:
98
99         (i) SEQUENCE CHARACTERISTICS:
100            (A) LENGTH: 17 base pairs
101            (B) TYPE: nucleic acid
102            (C) STRANDEDNESS: single
```

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RAW SEQUENCE LISTING
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TIME: 14:46:45

INPUT SET: S1104.raw

```
103              (D)  TOPOLOGY: linear
104
105       (ii)  MOLECULE TYPE: DNA (genomic)
106
107       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:5:
108
109  GTTTTCCCAG TCACGAC                                         17
110
111  (2)  INFORMATION FOR SEQ ID NO:6:
112
113        (i)  SEQUENCE CHARACTERISTICS:
114              (A)  LENGTH: 20 base pairs
115              (B)  TYPE: nucleic acid
116              (C)  STRANDEDNESS: single
117              (D)  TOPOLOGY: linear
118
119       (ii)  MOLECULE TYPE: DNA (genomic)
120
121       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:6:
122
123  GCGTCAGGGT GCTGCTGAGG                                      20
124
125   (2)  INFORMATION FOR SEQ ID NO:7:
126
127        (i)  SEQUENCE CHARACTERISTICS:
128              (A)  LENGTH: 20 base pairs
129              (B)  TYPE: nucleic acid
130              (C)  STRANDEDNESS: single
131              (D)  TOPOLOGY: linear
132
133       (ii)  MOLECULE TYPE: DNA (genomic)
134
135       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:7:
136
137  GGCGGGAAGA TGAAGACAGA                                      20
138
139  (2)  INFORMATION FOR SEQ ID NO:8:
140
141        (i)  SEQUENCE CHARACTERISTICS:
142              (A)  LENGTH: 20 base pairs
143              (B)  TYPE: nucleic acid
144              (C)  STRANDEDNESS: single
145              (D)  TOPOLOGY: linear
146
147       (ii)  MOLECULE TYPE: DNA (genomic)
148
149
150
151       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:8:
152
153  TTCAGCAGGC ACACAACAGA                                      20
```

```
154
155      (2) INFORMATION FOR SEQ ID NO:9:
156
157          (i) SEQUENCE CHARACTERISTICS:
158              (A) LENGTH: 1617 base pairs
159              (B) TYPE: nucleic acid
160              (C) STRANDEDNESS: both
161              (D) TOPOLOGY: linear
162
163         (ii) MOLECULE TYPE: cDNA
164
165        (iii) HYPOTHETICAL: NO
166
167         (iv) ANTI-SENSE: NO
168
169
170         (ix) FEATURE:
171              (A) NAME/KEY: sig_peptide
172              (B) LOCATION: 35..92
173
174         (ix) FEATURE:
175              (A) NAME/KEY: mat_peptide
176              (B) LOCATION: 93..1465
177
178         (ix) FEATURE:
179              (A) NAME/KEY: CDS
180              (B) LOCATION: 35..1465
181
182
183         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
184
185   TCTAAAGAAG CCCCTGGGAG CACAGCTCAT CACC ATG GAC TGG ACC TGG AGG      52
186                                         Met Asp Trp Thr Trp Arg
187                                         -19                 -15
188
189   TTC CTC TTT GTG GTG GCA GCA GCT ACA GGT GTC CAG TCC CAG ATG CAG    100
190   Phe Leu Phe Val Val Ala Ala Ala Thr Gly Val Gln Ser Gln Met Gln
191             -10                 -5                  1
192
193   GTG GTG CAG TCT GGG GCT GAA GTA AAG AAG CCT GGG TCC TCG GTG ACG    148
194   Val Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Thr
195         5                   10                  15
196
197   GTC TCC TGC AAG GCA TCT GGA GGC ACC TTC AGC AAC TAT GCT ATC AGC    196
198   Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr Ala Ile Ser
199    20                  25                  30                  35
200
201   TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC    244
202   Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile
203                       40                  45                  50
204
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205   ATC CCT CTT TTT GGT ACA CCA ACC TAC TCA CAG AAC TTC CAG GGC AGA        292
206   Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser Gln Asn Phe Gln Gly Arg
207               55                      60                      65
208
209   GTC ACG ATT ACC GCG GAC AAA TCC ACC AGC ACA GCC CAC ATG GAG CTG        340
210   Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala His Met Glu Leu
211               70                      75                      80
212
213   ACT AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT GCG ACA GAT        388
214   Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr Asp
215               85                      90                      95
216
217   CGC TAC AGG CAG GCA AAT TTT GAC CGG GCC CGG GTT GGC TGG TTC GAC        436
218   Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala Arg Val Gly Trp Phe Asp
219   100                     105                     110               115·
220
221   CCC TGG GGC CAG GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG        484
222   Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
223                   120                     125                     130
224
225   GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG        532
226   Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
227   `               135                     140                     145
228
229   GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG        580
230   Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
231               150                     155                     160
232
233   GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC        628
234   Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
235       165                     170                     175
236
237   TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG        676
238   Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
239   180                     185                     190               195
240
241   GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC        724
242   Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
243                   200                     205                     210
244
245   GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC        772
246   Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
247                   215                     220                     225
248
249   AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA        820
250   Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
251               230                     235                     240
252
253   CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC        868
254   Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
255       245                     250                     255
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256
257   ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC      916
258   Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
259   260                 265                 270                 275
260
261    GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC      964
262   Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
263                 280                 285                 290
264
265   GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC      1012
266   Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
267                 295                 300                 305
268
269   AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG      1060
270   Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
271                 310                 315                 320
272
273   CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA      1108
274   Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
275        325                 330                 335
276
277   GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA      1156
278   Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
279   340                 345                 350                 355
280
281   CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC      1204
282   Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
283                 360                 365                 370
284
285   CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC      1252
286   Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
287                 375                 380                 385
288
289   GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC      1300
290   Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
291                 390                 395                 400
292
293   ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG      1348
294   Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
295        405                 410                 415
296
297   CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC      1396
298   Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
299   420                 425                 430                 435
300
301   TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC      1444
302   Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
303                 440                 445                 450
304
305   TCC CTG TCT CCG GGT AAA TGAGTGCGAC GGCCGGCAAG CCCCCGCTCC            1492
306   Ser Leu Ser Pro Gly Lys
```

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307                    455
308
309    CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCGTGTACAT ACTTCCCGGG      1552
310
311    CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAAA AAAAAAAAAA      1612
312
313    AAAAA                                                                  1617
314    (2)  INFORMATION FOR SEQ ID NO:10:
315
316         (i)  SEQUENCE CHARACTERISTICS:
317              (A)  LENGTH: 476 amino acids
318              (B)  TYPE: amino acid
319              (D)  TOPOLOGY: linear
320
321         (ii)  MOLECULE TYPE: protein
322
323         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:10:
324
325    Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
326    -19             -15                 -10                     -5
327
328    Val Gln Ser Gln Met Gln Val Val Gln Ser Gly Ala Glu Val Lys Lys
329              1             5                   10
330
331    Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
332         15                  20                  25
333
334    Ser Asn Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
335     30                  35                  40                  45
336
337    Glu Trp Met Gly Gly Ile Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser
338                  50                  55                  60
339
340    Gln Asn Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
341              65                  70                  75
342
343    Thr Ala His Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val
344              80                  85                  90
345
346    Tyr Tyr Cys Ala Thr Asp Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala
347         95                  100                 105
348
349    Arg Val Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
350    110                 115                 120                 125
351
352    Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
353                  130                 135                 140
354
355    Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
356              145                 150                 155
357
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358   Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
359           160         165                 170
360
361   Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
362       175             180                 185
363
364   Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
365   190                 195                 200                 205
366
367    Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
368                 210                 215                 220
369
370   Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
371               225             230                 235
372
373   Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
374       240             245                 250
375
376   Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
377       255             260                 265
378
379   Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
380   270                 275                 280                 285
381
382   Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
383               290                 295                 300
384
385   Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
386           305             310                 315
387
388   Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
389           320             325                 330
390
391   Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
392       335             340                 345
393
394   Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
395   350             355                 360                 365
396
397   Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
398               370             375                 380
399
400   Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
401           385             390                 395
402
403   Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
404       400             405                 410
405
406   Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
407       415             420                 425
408
```

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RAW SEQUENCE LISTING
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DATE: 07/29/93
TIME: 14:47:15

INPUT SET: S1104.raw

```
409    Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
410    430             435             440                 445
411
412    Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
413                    450             455
414
415
416       (2) INFORMATION FOR SEQ ID NO:11:
417
418          (i) SEQUENCE CHARACTERISTICS:
419                (A) LENGTH: 902 base pairs
420                (B) TYPE: nucleic acid
421                (C) STRANDEDNESS: both
422                (D) TOPOLOGY: linear
423
424         (ii) MOLECULE TYPE: cDNA
425
426        (iii) HYPOTHETICAL: NO
427
428         (iv) ANTI-SENSE: NO
429
430
431         (ix) FEATURE:
432                (A) NAME/KEY: CDS
433                (B) LOCATION: 32..739
434
435         (ix) FEATURE:
436                (A) NAME/KEY: mat_peptide
437                (B) LOCATION: 89..739
438
439         (ix) FEATURE:
440                (A) NAME/KEY: sig_peptide
441                (B) LOCATION: 32..86
442
443
444         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
445
446    CAAGAGGCAG CGCTCTCGGG ACGTCTCCAC C ATG GCC TGG GCT CTG CTG CTC        52
447                                      Met Ala Trp Ala Leu Leu Leu
448                                      -19             -15
449
450    CTC ACC CTC CTC ACT CAG GAC ACA GGG TCC TGG GCC CAG TCT GCC CTG      100
451    Leu Thr Leu Leu Thr Gln Asp Thr Gly Ser Trp Ala Gln Ser Ala Leu
452            -10                 -5                  1
453
454    ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC ACC ATC      148
455    Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile
456     5                  10                  15                  20
457
458    TCC TGC ACT GGA ACC AAC AAT GAT GTT GGG AGT TAT AAC CTT GTC TCC      196
459    Ser Cys Thr Gly Thr Asn Asn Asp Val Gly Ser Tyr Asn Leu Val Ser
```

```
460                     25                  30                  35
461
462   TGG TAC CAG CAG CAC CCA GGC AAA GCC CCC AAA ATC ATG ATT TAT GAG        244
463   Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Ile Met Ile Tyr Glu
464                  40                  45                  50
465
466   GTC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC TCC AAG        292
467   Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys
468                  55                  60                  65
469
470   TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT GAG GAC        340
471   Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp
472                  70                  75                  80
473
474   GAG GCT GAT TAT TAC TGC TGC TCA TAT GCA GGT AGT TAC ACT GTG GTT        388
475   Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser Tyr Thr Val Val
476   85                  90                  95                  100
477
478   TTC GGC GGA GGG ACC AAA CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC        436
479   Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
480                  105                 110                 115
481
482   CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG CTT CAA GCC AAC        484
483   Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
484                  120                 125                 130
485
486   AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG        532
487   Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
488                  135                 140                 145
489
490   ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG        580
491   Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
492                  150                 155                 160
493
494   ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC        628
495   Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
496   165                 170                 175                 180
497
498   TAT CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC        676
499   Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
500                  185                 190                 195
501
502   TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT        724
503   Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
504                  200                 205                 210
505
506   ACA GAA TGT TCA TAGGTTCTAA ACCCTCACCC CCCCCACGGG AGACTAGAGC            776
507   Thr Glu Cys Ser
508                  215
509
510   TGCAGGATCC CAGGGGAGGG GTCTCTCCTC CCACCCCAAG GCATCAAGCC CTTCTCCCTG       836
```

511
512 CACTCAATAA ACCCTCAATA AATATTCTCA TTGTCAATCA CAAAAAAAAA AAAAAAAAAA   896
513
514 AAAAAA   902
515
516
517   (2) INFORMATION FOR SEQ ID NO:12:
518
519   (i) SEQUENCE CHARACTERISTICS:
520   (A) LENGTH: 235 amino acids
521   (B) TYPE: amino acid
522   (D) TOPOLOGY: linear
523
524   (ii) MOLECULE TYPE: protein
525
526   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
527
528 Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr Gly
529 -19   -15   -10   -5
530
531 Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
532   1   5   10
533
534 Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asp Val
535   15   20   25
536
537 Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
538 30   35   40   45
539
540 Pro Lys Ile Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser
541   50   55   60
542
543 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
544   65   70   75
545
546 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
547   80   85   90
548
549 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
550   95   100   105
551
552 Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
553 110   115   120   125
554
555 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
556   130   135   140
557
558 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
559   145   150   155
560
561 Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn

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RAW SEQUENCE LISTING
PATENT APPLICATION   US/07/952,640A

DATE: 07/29/93
TIME: 14:47:35

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562                160                  165                  170
563
564    Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
565        175                  180                  185
566
567    Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
568    190                  195                  200                  205
569
570    Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
571                210                  215         (2) INFORMATION FOR SEQ ID NO:13:
572
573         (i)  SEQUENCE CHARACTERISTICS:
574              (A)  LENGTH: 321 base pairs
575              (B)  TYPE: nucleic acid
576              (C)  STRANDEDNESS: both
577              (D)  TOPOLOGY: linear
578
579        (ii)  MOLECULE TYPE: cDNA
580
581       (iii)  HYPOTHETICAL: NO
582
583        (iv)  ANTI-SENSE: NO
584
585
586        (ix)  FEATURE:
587              (A)  NAME/KEY: CDS
588              (B)  LOCATION: 1..321
589
590
591        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:13:
592
593    GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA        48
594    Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
595     1               5                  10                  15
596
597    GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT        96
598    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
599                20                  25                  30
600
601    TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC       144
602    Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
603                35                  40                  45
604
605    TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC ACA TCA AGG TTC AGT GGC       192
606    Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
607        50                  55                  60
608
609    AGT GGA TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT       240
610    Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
611    65                  70                  75                  80
612
```

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613   GAA GAT TCT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG ATC      288
614   Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
615                   85                  90                  95
616
617   ACC TTC GGC CAA GGG ACA CGA CTG GAG ATT AAA                          321
618   Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
619                  100                 105
620
621
622   (2)  INFORMATION FOR SEQ ID NO:14:
623
624          (i)  SEQUENCE CHARACTERISTICS:
625                 (A)  LENGTH: 107 amino acids
626                 (B)  TYPE: amino acid
627                 (D)  TOPOLOGY: linear
628
629        (ii)  MOLECULE TYPE: protein
630
631        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:14:
632
633   Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
634    1               5                  10                  15
635
636   Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
637                   20                  25                  30
638
639   Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
640              35                  40                  45
641
642   Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
643         50                  55                  60
644
645   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
646    65                  70                  75                  80
647
648   Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
649                   85                  90                  95
650
651   Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
652                  100                 105
653
654   (2)  INFORMATION FOR SEQ ID NO:15:
655
656          (i)  SEQUENCE CHARACTERISTICS:
657                 (A)  LENGTH: 324 base pairs
658                 (B)  TYPE: nucleic acid
659                 (C)  STRANDEDNESS: both
660                 (D)  TOPOLOGY: linear
661
662        (ii)  MOLECULE TYPE: cDNA
663
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664        (iii) HYPOTHETICAL: NO
665
666        (iv) ANTI-SENSE: NO
667
668
669        (ix) FEATURE:
670              (A) NAME/KEY: CDS
671              (B) LOCATION: 1..324
672
673
674        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
675
676   GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA        48
677   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
678    1                5                  10                  15
679
680   GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT        96
681   Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
682                20                  25                  30
683
684   TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT GAG CTC CTG ATC       144
685   Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
686            35                  40                  45
687
688   TAT GCT GCT TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC       192
689   Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
690        50                  55                  60
691
692   AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
693   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
694    65                  70                  75                  80
695
696   GAA GAT TCT GCA GTT TAT TAC TGT CAA CAC ACT TAT AGT GAC CCG TAC       288
697   Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
698                85                  90                  95
699
700   AGT TTT GGC CAG GGG ACC AAA GTG GAC ATC AAA CGA                       324
701   Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
702            100                 105
703
704
705   (2) INFORMATION FOR SEQ ID NO:16:
706
707        (i) SEQUENCE CHARACTERISTICS:
708              (A) LENGTH: 108 amino acids
709              (B) TYPE: amino acid
710              (D) TOPOLOGY: linear
711
712        (ii) MOLECULE TYPE: protein
713
714        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
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715
716   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
717    1               5                  10                  15
718
719   Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
720               20                  25                  30
721
722   Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
723           35                  40                  45
724
725   Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
726       50                  55                  60
727
728   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
729    65                  70                  75                  80
730
731   Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
732               85                  90                  95
733
734   Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
735           100                 105
736
737   (2)  INFORMATION FOR SEQ ID NO:17:
738
739       (i)  SEQUENCE CHARACTERISTICS:
740           (A)  LENGTH: 324 base pairs
741           (B)  TYPE: nucleic acid
742           (C)  STRANDEDNESS: both
743           (D)  TOPOLOGY: linear
744
745      (ii)  MOLECULE TYPE: cDNA
746
747     (iii)  HYPOTHETICAL: NO
748
749      (iv)  ANTI-SENSE: NO
750
751
752      (ix)  FEATURE:
753           (A)  NAME/KEY: CDS
754           (B)  LOCATION: 1..324
755
756
757      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:17:
758
759   GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCT TCT GTA GGA        48
760   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
761  · 1               5                  10                  15
762
763   GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGC ACT TAT        96
764   Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
765               20                  25                  30
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RAW SEQUENCE LISTING
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DATE: 07/29/93
TIME: 14:48:02

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766
767    TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC        144
768    Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
769        35                  40                  45
770
771    TAT TAT GCA AAC AGT TTG GCA AGT GGG GTC CCA TCA AGG TTC AGC GGC        192
772    Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
773        50                  55                  60
774
775    AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT        240
776    Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
777    65                  70                  75                  80
778
779    GAA GAT TCT GCA ACT TAT TAC TGT GGA CAG GGT AAT AGT TAC CCT CTC        288
780    Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
781                    85                  90                  95
782
783    ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                        324
784    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
785            100                 105
786
787
788    (2)  INFORMATION FOR SEQ ID NO:18:
789
790         (i)  SEQUENCE CHARACTERISTICS:
791              (A)  LENGTH: 108 amino acids
792              (B)  TYPE: amino acid
793              (D)  TOPOLOGY: linear
794
795         (ii)  MOLECULE TYPE: protein
796
797         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:18:
798
799    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
800      1                 5                  10                  15
801
802    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
803                20                  25                  30
804
805    Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
806            35                  40                  45
807
808    Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
809        50                  55                  60
810
811    Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
812    65                  70                  75                  80
813
814    Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
815                    85                  90                  95
816
```

```
817    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
818                100                     105
819
820    (2) INFORMATION FOR SEQ ID NO:19:
821
822        (i)  SEQUENCE CHARACTERISTICS:
823             (A)  LENGTH: 324 base pairs
824             (B)  TYPE: nucleic acid
825             (C)  STRANDEDNESS: both
826             (D)  TOPOLOGY: linear
827
828       (ii)  MOLECULE TYPE: cDNA
829
830      (iii)  HYPOTHETICAL: NO
831
832       (iv)  ANTI-SENSE: NO
833
834
835       (ix)  FEATURE:
836             (A)  NAME/KEY: CDS
837             (B)  LOCATION: 1..324
838
839
840       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:19:
841
842    GAC ATT CAG CTG ACC CAG TCT CCA TCC TCT CAG TCT GCA TCT GTA GGA        48
843    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly
844     1               5                   10                  15
845
846    GAC AGA GTG ACC ATT ACT TGC CAG GCG AGT CAA AGC CTT AGC AAT TAT        96
847    Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr
848                20                  25                  30
849
850    TTA AAT TGG TAT CAG CAG AAA CCA GGG AAA ATT CCT AAG CTC CTG ATC       144
851    Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
852                35                  40                  45
853
854    TAT AGG GCA TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC       192
855    Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
856        50                  55                  60
857
858    AGT GGA TCT GGG ACG GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
859    Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
860    65                  70                  75                  80
861
862    GAA GAT TTT GCC ACT TAT TAC TGT CAG CAT AAT TAT GGT ACC CCT CTC       288
863    Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu
864                85                  90                  95
865
866    ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                       324
867    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/07/952,640A*

DATE: 07/29/93
TIME: 14:48:16

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868                     100                     105
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871     (2)  INFORMATION FOR SEQ ID NO:20:
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873           (i)  SEQUENCE CHARACTERISTICS:
874                 (A)  LENGTH: 108 amino acids
875                 (B)  TYPE: amino acid
876                 (D)  TOPOLOGY: linear
877
878           (ii) MOLECULE TYPE: protein
879
880           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
881
882     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly
883      1               5                  10                  15
884
885     Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr
886                 20                  25                  30
887
888     Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
889             35                  40                  45
890
891     Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
892         50                  55                  60
893
894     Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
895      65                  70                  75                  80
896
897     Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu
898                 85                  90                  95
899
900     Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
901                 100                 105
902
903     (2)  INFORMATION FOR SEQ ID NO:21:
904
905           (i)  SEQUENCE CHARACTERISTICS:
906                 (A)  LENGTH: 324 base pairs
907                 (B)  TYPE: nucleic acid
908                 (C)  STRANDEDNESS: both
909                 (D)  TOPOLOGY: linear
910
911           (ii) MOLECULE TYPE: DNA (genomic)
912
913
914           (ix) FEATURE:
915                 (A)  NAME/KEY: CDS
916                 (B)  LOCATION: 1..324
917
918           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/07/952,640A*

DATE: 07/29/93
TIME: 14:48:22

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919
920   GACATTCAGC TGACCCAGTC TCCACTCTCC CTGCCCGTCA GTCTTGGAGA GTCGGCCTCC   60
921
922   ATCTCCTNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   120
923
924   NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNTCCCAGAC   180
925
926   AGGTTCACTG GCAGTGGGTC AGGCACTGAT TTCACACTGA AAATCAGCAG AGTGGAGGCT   240
927
928   GAGGATGTTG GGGTTTATTA CTGCATGCAA GCTCTTCGGT CTCCTTGGAC GTTCGGCCAA   300
929
930   GGGACCAAGG TGGAAATCAG ACGA   324
931
932
933   (2) INFORMATION FOR SEQ ID NO:22:
934
935   (i) SEQUENCE CHARACTERISTICS:
936   (A) LENGTH: 108 amino acids
937   (B) TYPE: amino acid
938   (D) TOPOLOGY: linear
939
940   (ii) MOLECULE TYPE: protein
941
942   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
943
944   Asp Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
945   1   5   10   15
946
947   Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
948   20   25   30
949
950   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
951   35   40   45
952
953   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Arg Phe Thr Gly
954   50   55   60
955
956   Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
957   65   70   75   80
958
959   Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Arg Ser Pro Trp
960   85   90   95
961
962   Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Arg
963   100   105
964
965   (2) INFORMATION FOR SEQ ID NO:23:
966
967   (i) SEQUENCE CHARACTERISTICS:
968   (A) LENGTH: 324 base pairs
969   (B) TYPE: nucleic acid

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970              (C)  STRANDEDNESS: both
971              (D)  TOPOLOGY: linear
972
973       (ii)  MOLECULE TYPE: cDNA
974
975      (iii)  HYPOTHETICAL: NO
976
977       (iv)  ANTI-SENSE: NO
978
979
980       (ix)  FEATURE:
981              (A)  NAME/KEY: CDS
982              (B)  LOCATION: 1..324
983
984
985       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:23:
986
987    GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA          48
988    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
989     1               5                  10                  15
990
991    GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT          96
992    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
993                20                  25                  30
994
995    TTA AGT TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CTC CTG ATC         144
996    Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
997                35                  40                  45
998
999    TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC         192
1000   Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1001        50                  55                  60
1002
1003   AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAA CCT         240
1004   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1005    65                  70                  75                  80
1006
1007   GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG GGT TAT GGT ACC CCG TAC         288
1008   Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1009                85                  90                  95
1010
1011   AGT TTT GGC CAG GGG ACC AAA GTG GAG ATC AAA CGA                         324
1012   Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1013               100                 105
1014
1015
1016   (2)  INFORMATION FOR SEQ ID NO:24:
1017
1018          (i)  SEQUENCE CHARACTERISTICS:
1019              (A)  LENGTH: 108 amino acids
1020              (B)  TYPE: amino acid
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1021                    (D)  TOPOLOGY: linear
1022
1023           (ii)  MOLECULE TYPE: protein
1024
1025           (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:24:
1026
1027   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1028    1               5                  10                  15
1029
1030   Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
1031               20                  25                  30
1032
1033   Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1034           35                  40                  45
1035
1036   Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1037       50                  55                  60
1038
1039   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1040    65                  70                  75                  80
1041
1042   Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1043               85                  90                  95
1044
1045   Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1046           100                 105
1047
1048    (2)  INFORMATION FOR SEQ ID NO:25:
1049
1050           (i)  SEQUENCE CHARACTERISTICS:
1051                   (A)  LENGTH: 324 base pairs
1052                   (B)  TYPE: nucleic acid
1053                   (C)  STRANDEDNESS: both
1054                   (D)  TOPOLOGY: linear
1055
1056           (ii)  MOLECULE TYPE: cDNA
1057
1058          (iii)  HYPOTHETICAL: NO
1059
1060           (iv)  ANTI-SENSE: NO
1061
1062
1063           (ix)  FEATURE:
1064                   (A)  NAME/KEY: CDS
1065                   (B)  LOCATION: 1..324
1066
1067
1068           (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:25:
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1070   GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA        48
1071   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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RAW SEQUENCE LISTING
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DATE: 07/29/93
TIME: 14:48:43

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1074   GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GAC ATT AGC AAT AAT        96
1075   Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
1076            20                25                30
1077
1078   TTA GTC TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC       144
1079   Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1080            35                40                45
1081
1082   TAT GCT GCA TCC AGA TTG CAA GAT GGG GTC CCA TCA AGG TTC AGC GGC       192
1083   Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
1084         50                55                60
1085
1086   AGT GGG TCT GGG ACC GAT TTC ACC CTC ACA ATT AAT CCT GTG GAA GCT       240
1087   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
1088   65                70                75                80
1089
1090   GAC GAT GCT GCG GAT TAC TAC TGT CTA CAG ACT AAG AGT TCT CCT CGG       288
1091   Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
1092                  85                90                95
1093
1094   ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGA                       324
1095   Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1096                  100               105
1097
1098
1099   (2)  INFORMATION FOR SEQ ID NO:26:
1100
1101        (i)  SEQUENCE CHARACTERISTICS:
1102             (A)  LENGTH: 108 amino acids
1103             (B)  TYPE: amino acid
1104             (D)  TOPOLOGY: linear
1105
1106        (ii)  MOLECULE TYPE: protein
1107
1108        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:26:
1109
1110   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1111    1                 5                10                15
1112
1113   Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
1114            20                25                30
1115
1116   Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1117            35                40                45
1118
1119   Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
1120         50                55                60
1121
1122   Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
```

```
1123    65                    70                    75                    80
1124
1125    Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
1126                    85                    90                    95
1127
1128    Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1129                    100                   105
1130
1131    (2) INFORMATION FOR SEQ ID NO:27:
1132
1133        (i) SEQUENCE CHARACTERISTICS:
1134            (A) LENGTH: 324 base pairs
1135            (B) TYPE: nucleic acid
1136            (C) STRANDEDNESS: both
1137            (D) TOPOLOGY: linear
1138
1139        (ii) MOLECULE TYPE: DNA (genomic)
1140
1141
1142        (ix) FEATURE:
1143            (A) NAME/KEY: CDS
1144            (B) LOCATION: 1..324
1145
1146        (ix) FEATURE:
1147            (A) NAME/KEY: mat_peptide
1148            (B) LOCATION: 31..324
1149
1150
1151        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
1152
1153    GACATTCAGC TGACCCAGTC TCCANNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN      60
1154
1155    NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN     120
1156
1157    NNNNNNNNNN NNCAGCCCTT GATTTATGAG GTTTCCAACC GGGCCTCTGG AGTCCCAGAC     180
1158
1159    AGGTTCAGTG GCAGTGGGTC GGACACTGAT TTCACACTCA AAATCAGCAG AGTGGAGGCT     240
1160
1161    GAGGATGTTG GGGTTTATTA CTGCATGCAA TATACACACA TTCCATTCAC TTTCGGCCCC     300
1162
1163    GGGACCAAAC TGGATATCAA ACGA                                            324
1164
1165    (2) INFORMATION FOR SEQ ID NO:28:
1166
1167        (i) SEQUENCE CHARACTERISTICS:
1168            (A) LENGTH: 108 amino acids
1169            (B) TYPE: amino acid
1170            (D) TOPOLOGY: linear
1171
1172        (ii) MOLECULE TYPE: protein
1173
```

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1174
1175
1176        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:28:
1177
1178        Asp Ile Gln Leu Thr Gln Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1179        1               5               10                  15
1180
1181        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1182                    20                  25                  30
1183
1184        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Pro Leu Ile
1185                    35                  40                  45
1186
1187        Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1188            50                  55                  60
1189
1190        Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1191        65                  70                  75                  80
1192
1193        Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1194                    85                  90                  95
1195
1196        Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1197                    100                 105
1198
1199
1200
1201
1202    (2)  INFORMATION FOR SEQ ID NO:29:
1203
1204        (i)  SEQUENCE CHARACTERISTICS:
1205              (A)  LENGTH: 324 base pairs
1206              (B)  TYPE: nucleic acid
1207              (C)  STRANDEDNESS: both
1208              (D)  TOPOLOGY: linear
1209
1210       (ii)  MOLECULE TYPE: cDNA
1211
1212      (iii)  HYPOTHETICAL: NO
1213
1214       (iv)  ANTI-SENSE: NO
1215
1216
1217       (ix)  FEATURE:
1218              (A)  NAME/KEY: CDS
1219              (B)  LOCATION: 1..324
1220
1221
1222       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:29:
1223
1224    GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA      48
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RAW SEQUENCE LISTING
PATENT APPLICATION   US/07/952,640A

DATE: 07/29/93
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1225    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1226     1               5                   10                  15
1227
1228    GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT        96
1229    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
1230                20                  25                  30
1231
1232    TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT CAG CCC TTG ATT       144
1233    Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile
1234                35                  40                  45
1235
1236    TAT GAG GTT TCC AAC CGG GCC TCT GGA GTC CCA GAC AGG TTC AGT GGC       192
1237    Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1238         50                  55                  60
1239
1240    AGT GGG TCG GAC ACT GAT TTC ACA CTC AAA ATC AGC AGA GTG GAG GCT       240
1241    Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1242    65                  70                  75                  80
1243
1244    GAG GAT GTT GGG GTT TAT TAC TGC ATG CAA TAT ACA CAC ATT CCA TTC       288
1245    Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1246                    85                  90                  95
1247
1248    ACT TTC GGC CCC GGG ACC AAA CTG GAT ATC AAA CGA                       324
1249    Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1250                    100                 105
1251
1252
1253    (2)  INFORMATION FOR SEQ ID NO:30:
1254
1255         (i)  SEQUENCE CHARACTERISTICS:
1256              (A)  LENGTH: 108 amino acids
1257              (B)  TYPE: amino acid
1258              (D)  TOPOLOGY: linear
1259
1260         (ii)  MOLECULE TYPE: protein
1261
1262         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:30
1263
1264    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1265     1               5                   10                  15
1266
1267    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
1268                20                  25                  30
1269
1270    Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile
1271                35                  40                  45
1272
1273    Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1274         50                  55                  60
1275
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RAW SEQUENCE LISTING
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TIME: 14:49:10

INPUT SET: S1104.raw

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1276     Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1277      65                  70                  75                  80
1278
1279     Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1280                          85                  90                  95
1281
1282     Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1283                      100                 105
1284
1285     (2) INFORMATION FOR SEQ ID NO:31
1286
1287         (i)  SEQUENCE CHARACTERISTICS:
1288              (A)  LENGTH: 324 base pairs
1289              (B)  TYPE: nucleic acid
1290              (C)  STRANDEDNESS: both
1291              (D)  TOPOLOGY: linear
1292
1293        (ii)  MOLECULE TYPE: cDNA
1294
1295       (iii)  HYPOTHETICAL: NO
1296
1297        (iv)  ANTI-SENSE: NO
1298
1299
1300        (ix)  FEATURE:
1301              (A)  NAME/KEY: CDS
1302              (B)  LOCATION: 1..324
1303
1304
1305        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:31
1306
1307     GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA        48
1308     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1309      1               5                   10                  15
1310
1311     GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT        96
1312     Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1313                      20                  25                  30
1314
1315     TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC       144
1316     Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1317                  35                  40                  45
1318
1319     TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC       192
1320     Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1321          50                  55                  60
1322
1323     AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
1324     Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1325      65                  70                  75                  80
1326
```

```
1327    GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC        288
1328    Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1329                    85              90              95

1330
1331    ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                        324
1332    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1333                100             105

1334
1335
1336    (2)  INFORMATION FOR SEQ ID NO:32
1337
1338         (i)  SEQUENCE CHARACTERISTICS:
1339              (A)  LENGTH: 108 amino acids
1340              (B)  TYPE: amino acid
1341              (D)  TOPOLOGY: linear
1342
1343        (ii)  MOLECULE TYPE: protein
1344
1345        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:32
1346
1347    Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1348     1               5               10              15

1349
1350    Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1351                20              25              30

1352
1353    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1354            35              40              45

1355
1356    Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1357        50              55              60

1358
1359    Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1360     65              70              75              80

1361
1362    Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1363                85              90              95

1364
1365    Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1366                100             105

1367
1368    (2)  INFORMATION FOR SEQ ID NO:33
1369
1370         (i)  SEQUENCE CHARACTERISTICS:
1371              (A)  LENGTH: 324 base pairs
1372              (B)  TYPE: nucleic acid
1373              (C)  STRANDEDNESS: both
1374              (D)  TOPOLOGY: linear
1375
1376        (ii)  MOLECULE TYPE: cDNA
1377
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1378   (iii) HYPOTHETICAL: NO
1379
1380   (iv) ANTI-SENSE: NO
1381
1382
1383   (ix) FEATURE:
1384   (A) NAME/KEY: CDS
1385   (B) LOCATION: 1..324
1386
1387
1388   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33
1389
1390   GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA   48
1391   Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1392   1   5   10   15
1393
1394   GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT   96
1395   Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1396   20   25   30
1397
1398   TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC   144
1399   Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1400   35   40   45
1401
1402   TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC   192
1403   Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1404   50   55   60
1405
1406   AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT   240
1407   Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1408   65   70   75   80
1409
1410   GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC   288
1411   Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1412   85   90   95
1413
1414   ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA   324
1415   Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1416   100   105
1417
1418
1419   (2) INFORMATION FOR SEQ ID NO:34
1420
1421   (i) SEQUENCE CHARACTERISTICS:
1422   (A) LENGTH: 108 amino acids
1423   (B) TYPE: amino acid
1424   (D) TOPOLOGY: linear
1425
1426   (ii) MOLECULE TYPE: protein
1427
1428   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

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1429
1430     Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1431      1               5                   10                  15
1432
1433     Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1434                  20                  25                  30
1435
1436     Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1437              35                  40                  45
1438
1439     Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1440          50                  55                  60
1441
1442     Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1443      65                  70                  75                  80
1444
1445     Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1446                  85                  90                  95
1447
1448     Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1449              100                 105
1450
1451     (2)  INFORMATION FOR SEQ ID NO:35:
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1453          (i)  SEQUENCE CHARACTERISTICS:
1454               (A)  LENGTH: 342 base pairs
1455               (B)  TYPE: nucleic acid
1456               (C)  STRANDEDNESS: both
1457               (D)  TOPOLOGY: linear
1458
1459          (ii) MOLECULE TYPE: cDNA
1460
1461
1462          (ix) FEATURE:
1463               (A)  NAME/KEY: CDS
1464               (B)  LOCATION: 1..342
1465
1466
1467          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
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1469     GAC ATT GTG ATG ACT CAG TCT CCA ACT TTC CTT GCT GTG ACA GCA AGT        48
1470     Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser
1471      1               5                   10                  15
1472
1473     AAG AAG GTC ACC ATT AGT TGC ACT GCC TCT GAG AGC CTT TAT TCA AGC        96
1474     Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser
1475                  20                  25                  30
1476
1477     AAA CAC AAG GTG CAC TAC TTG GCT TGG TAC CAG AAG AAA CCA GAG CAA       144
1478     Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln
1479              35                  40                  45
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1480
1481    TCT CCT AAA CTG CTG ATA TAC GGG GCA TCC AAC CGA TAC ATT GGG GTC        192
1482    Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val
1483         50                      55                  60
1484
1485    CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTG ACC        240
1486    Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1487    65                      70                  75                  80
1488
1489    ATC AGC AGT GTA CAG GTT GAA GAC CTC ACA CAT TAT TAC TGT GCA CAG        288
1490    Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln
1491                    85                      90                  95
1492
1493    TTT TAC AGC TAT CCT CTC ACG TTC GGT GCT GGG ACC AAG CTG GAG CTG        336
1494    Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
1495                    100                     105                 110
1496
1497    AAA CGG                                                              342
1498    Lys Arg
1499
1500
1501
1502    (2)  INFORMATION FOR SEQ ID NO:36:
1503
1504         (i)  SEQUENCE CHARACTERISTICS:
1505              (A)  LENGTH: 114 amino acids
1506              (B)  TYPE: amino acid
1507              (D)  TOPOLOGY: linear
1508
1509        (ii)  MOLECULE TYPE: protein
1510
1511        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:36:
1512
1513    Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser
1514     1                   5                  10                  15
1515
1516    Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser
1517                 20                      25                  30
1518
1519    Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln
1520             35                      40                  45
1521
1522    Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val
1523         50                      55                  60
1524
1525    Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1526    65                      70                  75                  80
1527
1528    Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln
1529                    85                      90                  95
1530
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1531    Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
1532                100                 105                 110
1533
1534    Lys Arg
1535
1536
1537    (2)  INFORMATION FOR SEQ ID NO:37:
1538
1539         (i)  SEQUENCE CHARACTERISTICS:
1540              (A)  LENGTH: 327 base pairs
1541              (B)  TYPE: nucleic acid
1542              (C)  STRANDEDNESS: both
1543              (D)  TOPOLOGY: linear
1544
1545        (ii)  MOLECULE TYPE: cDNA
1546
1547       (iii)  HYPOTHETICAL: NO
1548
1549        (iv)  ANTI-SENSE: NO
1550
1551
1552        (ix)  FEATURE:
1553              (A)  NAME/KEY: CDS
1554              (B)  LOCATION: 1..327
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1556
1557        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:37:
1558
1559    GCC CTC GTG ATG ACC CAG ACT CCA GCC TCC GTG TCT GCA GCT GTG GGA      48
1560    Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1561     1               5                  10                  15
1562
1563    GGC ACA GTC ACC ATC AAG TGC CAG GCC AGT GAG AAC ATT TAC AGC TCT      96
1564    Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
1565                20                  25                  30
1566
1567    TTA GCC TGG TAT CAG CAG AAA CCA GGG CAG CCT CCC AAG CTC CTG ATC     144
1568    Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1569                35                  40                  45
1570
1571    TAT GGT GCA TCC ACT CTG GCA TCT GGG GTC CCA TCG CGG TTC AAA GGC     192
1572    Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1573         50                  55                  60
1574
1575    AGT AGA TCT GGG ACA GAG TAC ACT CTC ACC ATC AGC GGC GTG CAG CGT     240
1576    Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
1577     65                  70                  75                  80
1578
1579    GAG GAT GCT GCC ACC TAC TAC TGT CTA GGC AGT GAT AGT AGT AGC GAT     288
1580    Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp
1581                85                  90                  95
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1582
1583      ACT GCT TTC GGC GGA GGG ACC GAG CTG GAG ATC CTA TGT              327
1584      Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys
1585              100                 105
1586
1587
1588      (2)  INFORMATION FOR SEQ ID NO:38:
1589
1590          (i)  SEQUENCE CHARACTERISTICS:
1591              (A)  LENGTH: 109 amino acids
1592              (B)  TYPE: amino acid
1593              (D)  TOPOLOGY: linear
1594
1595          (ii) MOLECULE TYPE: protein
1596
1597          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
1598
1599      Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1600       1               5                 10                15
1601
1602      Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
1603              20                  25                  30
1604
1605      Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1606              35                  40                  45
1607
1608      Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1609          50                  55                  60
1610
1611      Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
1612       65                  70                  75                  80
1613
1614      Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp
1615                  85                  90                  95
1616
1617      Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys
1618              100                 105
1619
1620      (2)  INFORMATION FOR SEQ ID NO:39:
1621
1622          (i)  SEQUENCE CHARACTERISTICS:
1623              (A)  LENGTH: 321 base pairs
1624              (B)  TYPE: nucleic acid
1625              (C)  STRANDEDNESS: both
1626              (D)  TOPOLOGY: linear
1627
1628          (ii) MOLECULE TYPE: cDNA
1629
1630          (iii) HYPOTHETICAL: NO
1631
1632          (iv) ANTI-SENSE: NO
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1635        (ix)  FEATURE:
1636               (A)  NAME/KEY: CDS
1637               (B)  LOCATION: 1..321
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1639
1640        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:39:
1641
1642    ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG        48
1643    Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1644     1               5                   10                  15
1645
1646    TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT        96
1647    Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1648                 20                  25                  30
1649
1650    CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG       144
1651    Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
1652                 35                  40                  45
1653
1654    GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC       192
1655    Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
1656         50                  55                  60
1657
1658    TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA       240
1659    Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
1660     65                  70                  75                  80
1661
1662    CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC       288
1663    His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1664                 85                  90                  95
1665
1666    GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG                           321
1667    Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1668                 100                 105
1669
1670
1671     (2)  INFORMATION FOR SEQ ID NO:40:
1672
1673            (i)  SEQUENCE CHARACTERISTICS:
1674                   (A)  LENGTH: 106 amino acids
1675                   (B)  TYPE: amino acid
1676                   (D)  TOPOLOGY: linear
1677
1678          (ii)  MOLECULE TYPE: protein
1679
1680          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:40:
1681
1682    Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1683     1               5                   10                  15
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DATE: 07/29/93
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INPUT SET: S1104.raw

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1684
1685    Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1686                20                  25                  30
1687
1688    Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
1689            35                  40                  45
1690
1691    Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
1692        50                  55                  60
1693
1694    Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
1695    65                  70                  75                  80
1696
1697    His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1698                85                  90                  95
1699
1700    Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1701                100                 105
1702
1703
1704    (2)  INFORMATION FOR SEQ ID NO:41:
1705
1706        (i)  SEQUENCE CHARACTERISTICS:
1707            (A)  LENGTH: 321 base pairs
1708            (B)  TYPE: nucleic acid
1709            (C)  STRANDEDNESS: both
1710            (D)  TOPOLOGY: linear
1711
1712       (ii)  MOLECULE TYPE: cDNA
1713
1714      (iii)  HYPOTHETICAL: YES
1715
1716       (iv)  ANTI-SENSE: NO
1717
1718
1719       (ix)  FEATURE:
1720            (A)  NAME/KEY: CDS
1721            (B)  LOCATION: 1..321
1722
1723
1724       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:41:
1725
1726    GCT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAG GAT CAG        48
1727    Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln
1728     1               5                   10                  15
1729
1730    GTG AAA TCT GGA ACT GTC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT        96
1731    Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1732                20                  25                  30
1733
1734    CCC AGA GAG GCC AGC GTA AAG TGG AAG GTG GAT GGT GCC CTC AAA ACG       144
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1735    Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
1736            35                  40                  45
1737
1738    GAT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AAC ACC        192
1739    Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
1740            50                  55                  60
1741
1742    TAC AGC CTG AGC AGC ACC CTG ACG CTG AGC AGC ACA GAC TAC CAG AGT        240
1743    Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
1744    65                  70                  75                  80
1745
1746    CAC AAT GTC TAT GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC        288
1747    His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1748                    85                  90                  95
1749
1750    GTC ACC AAG AGC TTC AAC AGG GGA GAG TGT TAG                            321
1751    Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1752            100                 105
1753
1754
1755    (2) INFORMATION FOR SEQ ID NO:42:
1756
1757        (i) SEQUENCE CHARACTERISTICS:
1758            (A) LENGTH: 106 amino acids
1759            (B) TYPE: amino acid
1760            (D) TOPOLOGY: linear
1761
1762        (ii) MOLECULE TYPE: protein
1763
1764        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
1765
1766    Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln
1767     1                  5                  10                  15
1768
1769    Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1770            20                  25                  30
1771
1772    Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
1773            35                  40                  45
1774
1775    Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
1776            50                  55                  60
1777
1778    Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
1779    65                  70                  75                  80
1780
1781    His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1782                    85                  90                  95
1783
1784    Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1785            100                 105
```

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1786
1787
1788     (2) INFORMATION FOR SEQ ID NO:43:
1789
1790         (i) SEQUENCE CHARACTERISTICS:
1791             (A) LENGTH: 321 base pairs
1792             (B) TYPE: nucleic acid
1793             (C) STRANDEDNESS: both
1794             (D) TOPOLOGY: linear
1795
1796        (ii) MOLECULE TYPE: cDNA
1797
1798       (iii) HYPOTHETICAL: NO
1799
1800        (iv) ANTI-SENSE: NO
1801
1802
1803        (ix) FEATURE:
1804             (A) NAME/KEY: CDS
1805             (B) LOCATION: 1..321
1806
1807
1808        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
1809
1810     GAT CCA ATT GCG CCT ACT GTC CTC CTC TTC CCA CCA TCT GCT GAT CAG        48
1811     Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1812      1               5                  10                  15
1813
1814     CTG ACA ACT GAA ACA GTC ACC ATC GTG TGC GTG GCA AAT AAA TTC CGT       96
1815     Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
1816              20                  25                  30
1817
1818     CCC AAT GAC ATC ACC GTC ACC TGG AAG GTG GAT GAC GAA ATC CAA CAG      144
1819     Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln
1820              35                  40                  45
1821
1822     AGC GGC TTC GAG AAC AGT ACA ACA CCG CAG AGC CCC GAG GAC TGT ACC      192
1823     Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr
1824          50                  55                  60
1825
1826     TAC AAC CTC AGC AGC ACT CTG TCA CTG ACC AAA GCA CAG TAC AAC AGC      240
1827     Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser
1828      65                  70                  75                  80
1829
1830     CAC AGC GTG TAC ACC TGC GAG GTG GTC CAT CAC AAC TCG GGC TCA GCG      288
1831     His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala
1832                      85                  90                  95
1833
1834     ATC GTC CAG AGC TTC AAT AGG GGT GAC TGT TAG                          321
1835     Ile Val Gln Ser Phe Asn Arg Gly Asp Cys
1836                     100                 105
```

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1837
1838
1839        (2)  INFORMATION FOR SEQ ID NO:44:
1840
1841             (i)  SEQUENCE CHARACTERISTICS:
1842                  (A)  LENGTH: 106 amino acids
1843                  (B)  TYPE: amino acid
1844                  (D)  TOPOLOGY: linear
1845
1846            (ii)  MOLECULE TYPE: protein
1847
1848            (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:44:
1849
1850   Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1851    1               5                  10                  15
1852
1853   Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
1854               20                  25                  30
1855
1856   Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln
1857           35                  40                  45
1858
1859   Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr
1860           50                  55                  60
1861
1862   Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser
1863    65                  70             ·      75                  80
1864
1865   His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala
1866               85                  90                  95
1867
1868   Ile Val Gln Ser Phe Asn Arg Gly Asp Cys
1869           100                 105
1870
1871
1872
1873        (2)  INFORMATION FOR SEQ ID NO:45:
1874
1875             (i)  SEQUENCE CHARACTERISTICS:
1876                  (A)  LENGTH: 321 base pairs
1877                  (B)  TYPE: nucleic acid
1878                  (C)  STRANDEDNESS: both
1879                  (D)  TOPOLOGY: linear
1880
1881            (ii)  MOLECULE TYPE: cDNA
1882
1883           (iii)  HYPOTHETICAL: NO
1884
1885            (iv)  ANTI-SENSE: NO
1886
1887
```

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1888          (ix)  FEATURE:
1889                (A)  NAME/KEY: CDS
1890                (B)  LOCATION: 1..321
1891
1892
1893          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:45:
1894
1895     GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT GAG CAG          48
1896     Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
1897      1               5                  10                  15
1898
1899     TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC TTC TTG AAC AAC TTC TAC          96
1900     Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
1901                  20                  25                  30
1902
1903     CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT GAT GGC AGT GAA CGA CAA         144
1904     Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
1905                  35                  40                  45
1906
1907     AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG GAC AGC AAA GAC AGC ACC         192
1908     Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
1909          50                  55                  60
1910
1911     TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC AAG GAC GAG TAT GAA CGA         240
1912     Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
1913      65                  70                  75                  80
1914
1915     CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC AAG ACA TCA ACT TCA CCC         288
1916     His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
1917                  85                  90                  95
1918
1919     ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT TAG                             321
1920     Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
1921                  100                 105
1922
1923
1924     (2)  INFORMATION FOR SEQ ID NO:46:
1925
1926          (i)  SEQUENCE CHARACTERISTICS:
1927                (A)  LENGTH: 106 amino acids
1928                (B)  TYPE: amino acid
1929                (D)  TOPOLOGY: linear
1930
1931          (ii)  MOLECULE TYPE: protein
1932
1933          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:46:
1934
1935     Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
1936      1               5                  10                  15
1937
1938     Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
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1939                    20                      25                      30
1940
1941    Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
1942            35                      40                      45
1943
1944    Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
1945            50                      55                      60
1946
1947    Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
1948    65                      70                      75                      80
1949
1950    His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
1951                    85                      90                      95
1952
1953    Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
1954            100                     105
1955
1956
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1104.raw

Line	Error	Original Text		
27	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/952640		
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
571	Wrong Amino Acid Designator	210	215	(2) INFORMATION FOR SEQ ID N
591	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:		
10	Number of Sequences Doesn't Equal Actual	(iii) NUMBER OF SEQUENCES: 46		

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1104.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/07/952,640A*

INPUT SET: SI104.raw

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I262	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1285	(2) INFORMATION FOR SEQ ID NO:3I	(2) INFORMATION FOR SEQ ID NO:31:
1305	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
1336	(2) INFORMATION FOR SEQ ID NO:32	(2) INFORMATION FOR SEQ ID NO:32:
1345	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
1368	(2) INFORMATION FOR SEQ ID NO:33	(2) INFORMATION FOR SEQ ID NO:33:
1388	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
1419	(2) INFORMATION FOR SEQ ID NO:34	(2) INFORMATION FOR SEQ ID NO:34:
1428	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1112.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/952640

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/07/952,640A*

INPUT SET: S1112.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION   *US/07/952,640A*

INPUT SET: S1112.raw

Line	Original Text	Corrected Text
1264	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1287	(2) INFORMATION FOR SEQ ID NO:31	(2) INFORMATION FOR SEQ ID NO:31:
1307	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
1338	(2) INFORMATION FOR SEQ ID NO:32	(2) INFORMATION FOR SEQ ID NO:32:
1347	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
1370	(2) INFORMATION FOR SEQ ID NO:33	(2) INFORMATION FOR SEQ ID NO:33:
1390	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
1421	(2) INFORMATION FOR SEQ ID NO:34	(2) INFORMATION FOR SEQ ID NO:34:
1430	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: